

OY	1	MeGlnPheSerIaIaIeuIeaIaIeuValaIaIaGlyIleuAaSerIaGlnIeu	20
Db	152	ATCAATCTCTCAACCTCTCATGCTCTGTCGCTGCGAGCTGCCAGTGCACAGTC	211
OY	21	ProAspIleProProCySaIaIeuAncySphaValGluAaIeuGlyAAsnAspGlyCyS	40
Db	212	CCGAGATCCACCTTGGCCTCTCACTGCTTGTAAGCTCTCGGCAAGATGGCTGC	272
OY	41	ThiArgIeuThraSphPheCySAsySerySProGluIeuProGlyGlnIleThr	60
Db	272	ACCGCTTACCACTTCAGTGCACACTCTCCAAAGCTCCAGACTCCAGACAATCACT	333
OY	61	ProCyValaGluGluAaCySProIeuAspAaArgIleSerValSerAsnIleValaI	80
Db	332	CCTTGGCTGAGAGAGCCTGCCCTCGACGCCGGAATCTCGGTCCAACTGGTGTT	392
OY	81	AspGlnCySeryValaGlyValProIleAspIleProProValaAspThrThraIaA	100
Db	392	GACCAATGCTCAAGCCGAGCTGTCACATATGACATCCACAGTTGACACACCGCGCT	451

BASE COUNT	252 a	383 c	277 g	322 t
ORIGIN	/note="21 A nucleotides"			

### Alignment Scores:

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source
1. .1435
/organism="Coccidioides posadasii"
/mol_type="genomic DNA"
/strain="Silveira"
/db_xref="cazon:19306"
join(175. .255,334. .472,575. .939)
/codon_start=1
/product="antigen 2"
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//db_xref="GI:1256444"
/translation="WQSHALIALVAAGLASAQLPDIPECALNCFEALGNDGCTRLTT
DFKCHSKPELPQGITPVEAEACPLDARISVSIIVDOCSKACVPIDIPVDVTTAAPE
PSTIAETAPTEPTAEPTAEPTAEPTAEPTAEPTAEPTAEPTAEPTAEPTAEPTAEPT
PTASTAEFGAGSNSTRAASVGGIAAALLGAAVLT"
BASE COUNT      333 a      414 c      327 g      361 t
ORIGIN
Alignment Scores:
Pred. No.:      2.3e-48
Score:          970.00
Percent Similarity: 76.38%
Best Local Similarity: 75.98%
Query Match:    94.82%
DB:             8 Gaps: 2

```

05	10	-061-933-4	(1-194)	X	CU051200	(1-1435)	
QY	1	MetGlnPheSerHisAlaLeuIleAlaLeuValAlaAlaGlyLeuAlaSerAlaGlnLeu	20				
Db	175	ATCAGATTCTCTCAACGCTCTCAATCGCTCTGTGTGCTGCGCGCTCGGCATGCCCCAGTCTC	234				
QY	21	ProAspIleProProCysAla-----	27				
Db	235	CCAGACATCCCACTTCGCGCTGTATGTCGAACTTTGTGTGAACTCAGCGAGAGGA	294				
QY	28	-----LeuAnCysPheValGluAla	34				
Db	295	ACGAGAAGCACTCTTGGAATGCTAACGCGCTTATGCTAGCTCAACTGCTTCGTGAGAGCT	354				
QY	35	LeuGlyAsnAspGlyCysThrArgLeuThrAspPheIleCysHisIacCysSerIleProGlu	54				
Db	355	CTGGCGAAGATGGCTGCACTCGCTTGACGGAATTCAAGGCCACTGCTCCAAAGCGCTGAG	414				
QY	55	LeuProGlyGlnIleThrProCysValGluGluAlaCysProLeuAsnAlaArgIle---	73				
Db	415	CTCCCAAGACAGATCACTCTTCGCTGTGAGAGAGGCTGCCTCTCGACGCCCGATCTGT	474				
QY	73	-----	73				

D	b		473	AAGTGAAGCAACCAAATTTCTTGACTTCGGCCCAAGATTGGATAAGATGAGAATGC	534
Q	y		74	-----SerValSerAsnIleVal180 :::	
D	b		535	AAAGAAGTCGAATGGCAGCTAACATGTTAAAAAATCCAGCGCTCTCCAACTCGTCGT	594
Q	y		81	AAPGLCYseSerIyeAlaglyValProIIeapPIIeoproProvalAspThrThralala	100
D	b		595	GACCAATGTCTCCAAAGGCCGTGTCCCAATGTGATCATCCACCAGTTATACACCAACCGCGCT	654
Q	y		101	ProGIuProSeclunThralagiupProThralagiupProThngluInubProThralagi	120
D	b		655	CCCGAGCCATCCGAGACCCGCTAGGCCACCGCTGAGCCAAACGAGAGCCCACTGCCGAG	714
Q	y		121	ProThralagiupProThralagiupProThrriagiupProThrgluInubProThralaVal	140
D	b		715	CCTAACGCTGAGGCCCAACGCTGAGCCGACTCATAGGCCCAACGAGAGGCCCACTGCCCTC	774
Q	y		141	ProThnglyThnclyglVglValProThrglyThnglySePheThrValThrglyArg	160
D	b		775	CCAACCGGACATGGGGGTGTCTCCCACTGGCACCGGTTCTTCCATCCCTCACTGGCAAA	834
Q	y		161	ProThralaseThrProalaginupheProgiyalagiSerAsnValarglaserVal	180